

SEQUENCE LISTING

<110> Fibrogen, Inc.
Grotendorst, Gary
Neff, Thomas

<120> Connective Tissue Growth Factor Fragments and Methods and Uses Thereof

<130> FIBRO1130-2

<140> 09/461,646

<141> 1999-12-14

<150> 60/112,240

<151> 1998-12-14

<150> 60/112,241

<151> 1998-12-14

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 2075

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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gtgccaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc gtg 171

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val

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gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc agc 219

Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser

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ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg ggc 267

Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly

35 40 45

gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc aag 315

Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys

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cag ctg ggc gag ctg tgc acc gag cgc gac ccc tgc gac ccg cac aag 363

Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys

65 70 75

ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac cgc aag atc ggc gtg 411

Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val

80 85 90

tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg tac 459

Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr

95 100 105 110

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ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc aag ctg ccc ggg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly 145 150 155	603
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gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys 240 245 250	891
aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu 255 260 265 270	939
tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val 275 280 285	987
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ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp 320 325 330	1131
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gggaaaagat tcccacccaa ttcaaaacat tgtgccatgt caaacaata gtctatcttc	1356

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 35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130 135 140
 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145 150 155 160
 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165 170 175
 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180 185 190
 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195 200 205
 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210 215 220
 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225 230 235 240
 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245 250 255
 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260 265 270
 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275 280 285
 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290 295 300
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
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Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys	
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tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc aat gac aac	144
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn	
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gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg gtc agg cct	192
Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro	
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Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile	
65 70 75 80	
cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt tct ggc tgc	288
Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly Cys	
85 90 95	
acc agc atg aag aca tac cga gct aaa ttc tgt gga gta tgt acc gac	336
Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp	
100 105 110	
ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg gtg gag ttc	384
Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe	
115 120 125	
aag tgc cct gac ggc gag gtc atg aag aag aac atg atg ttc atc aag	432
Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile Lys	
130 135 140	
acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac atc ttt gaa	480
Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu	
145 150 155 160	
tcg ctg tac tac agg aag atg tac gga gac atg gca tgaagccaga	526
Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala	
165 170	
gagtgcagaga cattaactca ttagactgga acttgaactg attcacatct catttttccg	586
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tgaatttgcc tgtaacaagc cagattttttt aaaatttata ttgtaaatat tgtgtgtgtg	1126

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 35 40 45

Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
 50 55 60

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
 65 70 75 80

Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly Cys
 85 90 95

Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
 100 105 110

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
 115 120 125

Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile Lys
 130 135 140

Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
 145 150 155 160

Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 165 170